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1: FEMS Microbiol Lett 1992 Apr 1;71(1):23-7

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Fine-structure mapping of cis-acting control sites in the *lysC* operon of *Bacillus subtilis*.

Lu Y, Shevtchenko TN, Paulus H.

Department of Metabolic Regulation, Boston Biomedical Research Institute, MA 02114.

Mutations at the *aecA* locus of *Bacillus subtilis* lead to derepression of the *lysC* operon, which encodes aspartokinase II, and analysis of three independent *aecA* mutations has shown them to be nucleotide substitutions in the *lysC* leader region (Y. Lu, N.Y. Chen and H. Paulus (1991) J. Gen. Microbiol. 137, 1135-1141). DNA sequence analysis of the *lysC* control region of nine other mutants with derepressed levels of aspartokinase II revealed each of the mutations to be associated with changes in one or a few nucleotide residues. The nucleotide substitutions were clustered at two sites in the *lysC* leader: in a region of imperfect dyad symmetry about 40 base pairs from the transcription start site, and in the open reading frame for a putative leader peptide, which starts about 40 residues further downstream. The effect of nucleotide substitutions at the two sites differed in that those at the upstream site gave twice the degree of derepression. A mutant with a small deletion in the leader peptide coding region potentially affecting RNA secondary structure also had a higher level of *lysC* derepression. These results suggest that the *lysC* leader region contains at least two cis-acting control sites that play important and perhaps independent roles in the repression of the *lysC* operon by lysine.

PMID: 1624109 [PubMed - indexed for MEDLINE]

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1: NP_803887

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aspartokinase I; homoserine dehydrogenase I [Salmonella enterica subsp.
enterica serovar Typhi Ty2]
gi|29140545|ref|NP_803887.1|[29140545]

2: AAO67736

BLink, Links

aspartokinase I; homoserine dehydrogenase I [Salmonella enterica subsp.
enterica serovar Typhi Ty2]
gi|29136169|gb|AAO67736.1|[29136169]

3: NP_240025

BLink, Domains, Links

aspartokinase I; homoserine dehydrogenase I [Buchnera sp. APS]
gi|15616813|ref|NP_240025.1|[15616813]

4: NP_751959

BLink, Domains, Links

Aspartokinase I; Homoserine dehydrogenase I [Escherichia coli CFT073]
gi|26245920|ref|NP_751959.1|[26245920]

5: AAN78503

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Aspartokinase I; Homoserine dehydrogenase I [Escherichia coli CFT073]
gi|26106317|gb|AAN78503.1|AE016755_3[26106317]

6: C64371

BLink, Domains, Links

aspartate kinase (EC 2.7.2.4) I - Methanococcus jannaschii
gi|2127773|pir||C64371[2127773]

7: AAL18966

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gi|16418495|gb|AAL18966.1|[16418495]

8: AAA22384

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aspartokinase I
gi|142829|gb|AAA22384.1|[142829]

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gi|15926973|ref|NP_374506.1|[15926973]
- [2](#): [NP_807165](#) [BLink](#), [Links](#)
aspartokinase II; homoserine dehydrogenase II [Salmonella enterica subsp.
enterica serovar Typhi Ty2]
gi|29143823|ref|NP_807165.1|[29143823]
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enterica serovar Typhi Ty2]
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AKII-HDII protein; Aspartokinase II; Homoserine dehydrogenase II
[Escherichia coli CFT073]
gi|26250707|ref|NP_756747.1|[26250707]
- [5](#): [BAB42485](#) [BLink](#), [Domains](#), [Links](#)
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gi|13701190|dbj|BAB42485.1|[13701190]
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aspartokinase II [Staphylococcus epidermidis ATCC 12228]
gi|27467991|ref|NP_764628.1|[27467991]
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gi|27315536|gb|AAO04670.1|AE016747_167|[27315536]
- [8](#): [AAN83321](#) [BLink](#), [Domains](#), [Links](#)
AKII-HDII protein; Aspartokinase II; Homoserine dehydrogenase II
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gi|26111138|gb|AAN83321.1|AE016770_121|[26111138]

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gi|21283010|ref|NP_646098.1|[21283010]
- └ **11: [NP_371917](#)** BLink, Domains, Links
aspartokinase II [Staphylococcus aureus subsp. aureus Mu50]
gi|15924383|ref|NP_371917.1|[15924383]
- └ **12: [NP_229318](#)** BLink, Domains, Links
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gi|15644266|ref|NP_229318.1|[15644266]
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gi|15643313|ref|NP_228357.1|[15643313]
- └ **14: [H72364](#)** BLink, Domains, Links
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gi|7462061|pir||H72364[7462061]
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gi|7434557|pir||G72245[7434557]
- └ **16: [JC4640](#)** BLink, Domains, Links
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gi|2126845|pir||JC4640[2126845]
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- └ **18: [BAB57555](#)** BLink, Domains, Links
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- └ **20: [AAG42244](#)** BLink, Domains, Links
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gi|4982084|gb|AAD36585.1|AE001799_17[4982084]

22: AAD35632

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23: AAA22251

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aspartokinase II
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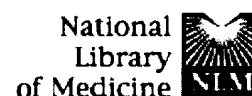
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- 1: [NP_824095](#) BLink, Links
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- 2: [NP_822091](#) BLink, Links
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gi|29827457|ref|NP_822091.1|[29827457]
- 3: [AAM65955](#) BLink, Domains, Links
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[Ralstonia solanacearum]
gi|17431150|emb|CAD17830.1|[17431150]
- 5: [1HKWB](#) BLink, Links
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- 6: [1HKWA](#) BLink, Links
Chain A, Mycobacterium Diaminopimelate Dicarboxylase (Lysa)
gi|29726282|pdb|1HKW|A[29726282]
- 7: [1HKVB](#) BLink, Links
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gi|29726281|pdb|1HKV|B[29726281]
- 8: [1HKVA](#) BLink, Links
Chain A, Mycobacterium Diaminopimelate Dicarboxylase (Lysa)
gi|29726280|pdb|1HKV|A[29726280]
- 9: [BAC70630](#) BLink, Links
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- └ **10:** [BAC68626](#) BLink, Links
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- └ **11:** [NP_633909](#) BLink, Domains, Links
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- └ **12:** [NP_613768](#) BLink, Domains, Links
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gi|20093921|ref|NP_613768.1|[20093921]
- └ **13:** [NP_394250](#) BLink, Domains, Links
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- └ **14:** [NP_248090](#) BLink, Domains, Links
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gi|15669285|ref|NP_248090.1|[15669285]
- └ **15:** [NP_111325](#) BLink, Domains, Links
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- └ **16:** [NP_069634](#) BLink, Domains, Links
diaminopimelate decarboxylase (lysA) [*Archaeoglobus fulgidus* DSM 4304]
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- └ **17:** [NP_815225](#) BLink, Links
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gi|29376071|ref|NP_815225.1|[29376071]
- └ **18:** [BAC66455](#) BLink, Links
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gi|29365470|dbj|BAC66455.1|[29365470]
- └ **19:** [CAB14270](#) BLink, Domains, Links
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gi|2634773|emb|CAB14270.1|[2634773]
- └ **20:** [NP_810287](#) BLink, Links
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gi|29346784|ref|NP_810287.1|[29346784]



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1: Arch Microbiol 1985 Mar;141(2):143-50

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Regulation of lysine and dipicolinic acid biosynthesis in *Bacillus brevis* ATCC 10068: significance of derepression of the enzymes during the change from vegetative growth to sporulation.

Rao AS.

Lysine biosynthetic pathway enzymes of *Bacillus brevis* ATCC 1068 were studied as a function of stage of development (growth and sporulation). The synthesis of aspartic-2-semialdehyde dehydrogenase (ASA-dehydrogenase), dihydrodipicolinate synthase (DHDPA-synthase), DHDPA-reductase and diaminopimelate decarboxylase (DAP-decarboxylase) was found not to be co-regulated, since lysine was not a co-repressor for these enzymes. Unlike the aspartokinase isoenzymes, the other enzymes of the lysine pathway were not derepressed in thiosine-resistant, lysine-excreting mutants. Thus, the aspartokinase isoenzymes were the key enzymes during growth and regulation of lysine biosynthesis through restriction of L-ASA synthesis via feedback control by lysine on the aspartokinases was therefore suggested. In contrast to other *Bacillus* species, the levels of the lysine biosynthetic pathway enzymes of strain ATCC 10068 were not derepressed during the change from vegetative growth to sporulation. Two control mechanisms, enabling the observed preferential channelling of carbon for the synthesis of spore-specific diaminopimelic acid (DAP) and dipicolinic acid (DPA) were a) loss of DAP-decarboxylase, b) inhibition of DHDPA-reductase by DPA. Increase in the level of the DAP pool during sporulation, as a consequence of the loss of DAP-decarboxylase, and its relevance to the non-enzymatic formation of DPA has been discussed.

PMID: 3922324 [PubMed - indexed for MEDLINE]

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